Geographically extensive larval surveys reveal an unexpected scarcity of primary vector mosquitoes in a region of persistent malaria transmission in western Zambia

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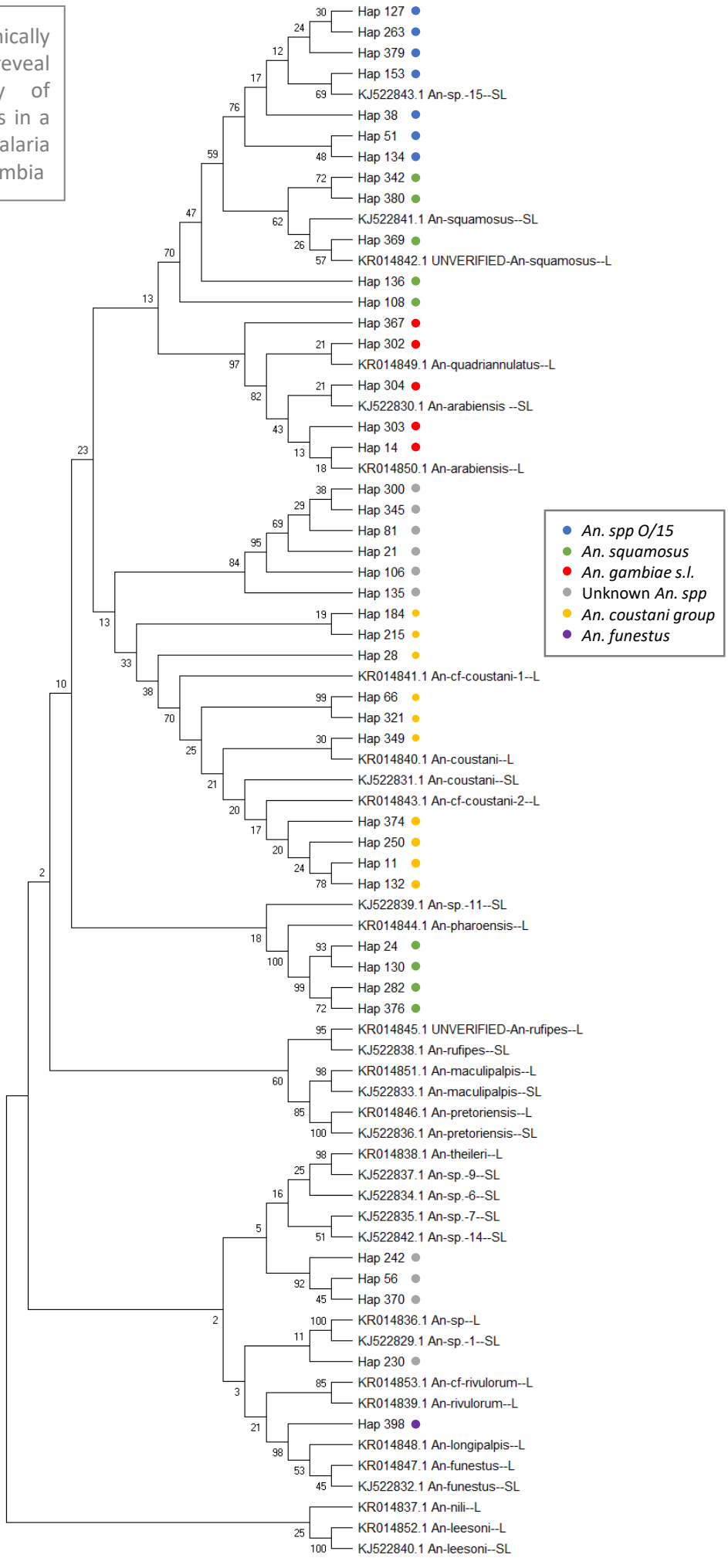

Figure S1: Maximum Likelihood phylogenetic tree of cytochrome *c* oxidase I (COI) sequences from *Anopheles* larvae sampled in western Zambia. Consensus tree constructed in MEGA X from a 318bp fragment of the COI region of mitochondrial DNA, using 100 bootstrap replicates. Sequences from this paper have been labelled with taxon assignment used in this paper. Published reference sequences are labelled with NCBI nt accession number and species ID; suffix denotes source paper. '**--L**' denotes Lobo *et al.* (2015); '**--SL**' denotes St Laurent *et al.* (2016).

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